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#2



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RAW SEQUENCE LISTING

DATE: 02/01/2002

PATENT APPLICATION: US/10/006,343

TIME: 11:47:30

Input Set : N:\Crf3\RULE60\10006343.raw

Output Set: N:\CRF3\02012002\J006343.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Bard, Jonathan A
6 Borowsky, Beth
7 Smith, Kelli E
9 (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
10 AND USES THEREOF
12 (iii) NUMBER OF SEQUENCES: 65
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Cooper & Dunham LLP
16 (B) STREET: 1185 Avenue of the Americas
17 (C) CITY: New York
18 (D) STATE: New York
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 10036
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/10/006,343
C--> 30 (B) FILING DATE: 03-Dec-2001
31 (C) CLASSIFICATION:
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US/09/058,333
36 (B) FILING DATE:
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: White, John P
42 (B) REGISTRATION NUMBER: 28,678
43 (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: 212 278 0400
47 (B) TELEFAX: 212 391 0525
50 (2) INFORMATION FOR SEQ ID NO: 1:
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 1280 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear
W--> 58 (ii) MOLECULE TYPE: DNA
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS

ENTERED

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62      (B) LOCATION: 63..1172
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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68 AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA      107
69 Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val
70      1      5      10      15
72 GGG GCT GTG GCA GTG CCT GTG ATC TTT GCC CTC ATC TTC CTG TTG GGC      155
73 Gly Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly
74      20      25      30
76 ATG GTG GGC AAT GGG CTG GTG TTG GCT GTG CTA CTG CAG CCT GGC CCA      203
77 Met Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro
78      35      40      45
80 AGT GCC TGG CAG GAG CCA AGC AGT ACC ACA GAT CTC TTC ATC CTC AAC      251
81 Ser Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn
82      50      55      60
84 TTG GCC GTG GCC GAC CTT TGC TTC ATC CTG TGC TGC GTG CCC TTC CAG      299
85 Leu Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln
86      65      70      75
88 GCA GCC ATC TAC ACA CTG GAT GCC TGG CTC TTT GGG GCT TTC GTG TGC      347
89 Ala Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys
90      80      85      90      95
92 AAG ACG GTA CAT CTG CTC ATC TAC CTC ACC ATG TAT GCC AGC AGC TTC      395
93 Lys Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe
94      100      105      110
96 ACC CTG GCG GCC GTC TCC CTG GAC AGG TAC CTG GCT GTG CGG CAC CCA      443
97 Thr Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro
98      115      120      125
100 CTG CGC TCC AGA GCC CTG CGC ACC CCG CGC AAC GCG CGC GCC GCC GTG      491
101 Leu Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val
102      130      135      140
104 GGG CTC GTG TGG CTG CTG GCG GCT CTC TTT TCC GCG CCC TAC CTA AGC      539
105 Gly Leu Val Trp Leu Leu Ala Leu Phe Ser Ala Pro Tyr Leu Ser
106      145      150      155
108 TAT TAC GGC ACG GTG CGC TAC GGC GCG CTC GAG CTC TGC GTG CCC GCT      587
109 Tyr Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala
110      160      165      170      175
112 TGG GAG GAC GCG CGG CGG CGC GCG CTG GAC GTG GCC ACC TTC GCC GCG      635
113 Trp Glu Asp Ala Arg Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala
114      180      185      190
116 GGC TAC CTG CTG CCG GTG GCC GTG GTG AGC CTG GCC TAC GGA CGC ACG      683
117 Gly Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr
118      195      200      205
120 CTA TGT TTC CTA TGG GCC GCC GTG GGT CCC GCG GGC GCG GCA GCA      731
121 Leu Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala
122      210      215      220
124 GAG GCG CGC AGA CGG GCG ACC GGC CGG GCG GGA CGC GCC ATG CTG GCA      779
125 Glu Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala
126      225      230      235
128 GTG GCC GCG CTC TAC GCG CTT TGC TGG GGC CCG CAC CAC GCG CTC ATC      827

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Input Set : N:\Crif3\RULE60\10006343.raw

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129 Val Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile
130 240 245 250 255
132 CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC 875
133 Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala
134 260 265 270
136 TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC 923
137 Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn
138 275 280 285
140 CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC 971
141 Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg
142 290 295 300
144 CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CAC CGC GCT 1019
145 Arg Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala
146 305 310 315
148 CAT CGA GCC CTC CGT CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT 1067
149 His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly
150 320 325 330 335
152 TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG 1115
153 Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly
154 340 345 350
156 GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG 1163
157 Asp Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg
158 355 360 365
160 GGA CCT CAA TAACCCTGCC CGCTTGACT CTGACGTCTG TCAGAATGCC 1212
161 Gly Pro Gln
162 370
164 ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG 1272
166 TTGCAGGG 1280
169 (2) INFORMATION FOR SEQ ID NO: 2:
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 370 amino acids
173 (B) TYPE: amino acid
174 (D) TOPOLOGY: linear
176 (ii) MOLECULE TYPE: protein
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
180 Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly
181 1 5 10 15
183 Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met
184 20 25 30
186 Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser
187 35 40 45
189 Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu
190 50 55 60
192 Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala
193 65 70 75 80
195 Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys Lys
196 85 90 95
198 Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr
199 100 105 110

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Input Set : N:\Crif3\RULE60\10006343.raw

Output Set: N:\CRF3\02012002\J006343.raw

```

201 Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
202      115      120      125
204 Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
205      130      135      140
207 Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
208 145      150      155      160
210 Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
211      165      170      175
213 Glu Asp Ala Arg Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
214      180      185      190
216 Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
217      195      200      205
219 Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala Glu
220      210      215      220
222 Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
223 225      230      235      240
225 Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
226      245      250      255
228 Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
229      260      265      270
231 Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
232      275      280      285
234 Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
235      290      295      300
237 Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala His
238 305      310      315      320
240 Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
241      325      330      335
243 Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
244      340      345      350
246 Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
247      355      360      365
249 Pro Gln
250      370

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253 (2) INFORMATION FOR SEQ ID NO: 3:

255 (i) SEQUENCE CHARACTERISTICS:

256 (A) LENGTH: 1417 base pairs

257 (B) TYPE: nucleic acid

258 (C) STRANDEDNESS: single

259 (D) TOPOLOGY: linear

W--> 261 (ii) MOLECULE TYPE: DNA

263 (ix) FEATURE:

264 (A) NAME/KEY: CDS

265 (B) LOCATION: 1..1281

268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

270 CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG 48

271 His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr

W--> 272 375 380 385

274 AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA 96

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Input Set : N:\Crf3\RULE60\10006343.raw

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	275	Ser	Phe	Gln	Pro	Arg	Thr	Pro	Gly	Gln	Thr	Gln	Val	Gly	Gly	Val	Arg	
W-->	276				390				395					400				
	278	TCC	CGG	GGT	CAA	GCA	ACC	AGA	ACT	GGG	GGC	TCT	TGC	CTG	AGG	ATT	CCA	144
	279	Ser	Arg	Gly	Gln	Ala	Thr	Arg	Thr	Gly	Gly	Ser	Cys	Leu	Arg	Ile	Pro	
W-->	280			405					410					415				
	282	GCT	TCT	CTT	CCC	AGG	TGC	CCG	TCT	GAT	GGG	GAG	ATG	GCT	GAT	GCC	CAG	192
	283	Ala	Ser	Leu	Pro	Arg	Cys	Pro	Ser	Asp	Gly	Glu	Met	Ala	Asp	Ala	Gln	
W-->	284		420						425					430				
	286	AAC	ATT	TCA	CTG	GAC	AGC	CCA	GGG	AGT	GTG	GGG	GCC	GTG	GCA	GTG	CCT	240
	287	Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val	Gly	Ala	Val	Ala	Val	Pro	
W-->	288	435					440					445				450		
	290	GTG	GTC	TTT	GCC	CTA	ATC	TTC	CTG	CTG	GGC	ACA	GTG	GGC	AAT	GGG	CTG	288
	291	Val	Val	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	Thr	Val	Gly	Asn	Gly	Leu	
W-->	292				455					460					465			
	294	GTG	CTG	GCA	GTG	CTC	CTG	CAG	CCT	GGC	CCG	AGT	GCC	TGG	CAG	GAG	CCT	336
	295	Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	Ser	Ala	Trp	Gln	Glu	Pro	
W-->	296			470					475					480				
	298	GGC	AGC	ACC	ACG	GAC	CTG	TTC	ATC	CTC	AAC	CTG	GCG	GTG	GCT	GAC	CTC	384
	299	Gly	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	
W-->	300			485					490					495				
	302	TGC	TTC	ATC	CTG	TGC	TGC	GTG	CCC	TTC	CAG	GCC	ACC	ATC	TAC	ACG	CTG	432
	303	Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	Ala	Thr	Ile	Tyr	Thr	Leu	
W-->	304		500					505					510					
	306	GAT	GCC	TGG	CTC	TTT	GGG	GCC	CTC	GTC	TGC	AAG	GCC	GTG	CAC	CTG	CTC	480
	307	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Leu	Val	Cys	Lys	Ala	Val	His	Leu	Leu	
W-->	308	515				520					525				530			
	310	ATC	TAC	CTC	ACC	ATG	TAC	GCC	AGC	AGC	TTT	ACG	CTG	GCT	GCT	GTC	TCC	528
	311	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr	Leu	Ala	Ala	Val	Ser	
W-->	312			535					540						545			
	314	GTG	GAC	AGG	TAC	CTG	GCC	GTG	CGG	CAC	CCG	CTG	CGC	TCG	CGC	GCC	CTG	576
	315	Val	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	Leu	Arg	Ser	Arg	Ala	Leu	
W-->	316			550					555					560				
	318	CGC	ACG	CCG	CGT	AAC	GCC	CGC	GCC	GCA	GTG	GGG	CTG	GTG	TGG	CTG	CTG	624
	319	Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	Gly	Leu	Val	Trp	Leu	Leu	
W-->	320			565					570					575				
	322	GCG	GCG	CTC	TTC	TCG	GCG	CCC	TAC	CTC	AGC	TAC	TAC	GGC	ACC	GTG	CGC	672
	323	Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	Tyr	Tyr	Gly	Thr	Val	Arg	
W-->	324		580					585					590					
	326	TAC	GGC	GCG	CTG	GAG	CTC	TGC	GTG	CCC	GCC	TGG	GAG	GAC	GCG	CGC	CGC	720
	327	Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	Trp	Glu	Asp	Ala	Arg	Arg	
W-->	328	595				600					605				610			
	330	CGC	GCC	CTG	GAC	GTG	GCC	ACC	TTC	GCT	GCC	GGC	TAC	CTG	CTG	CCC	GTG	768
	331	Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	Gly	Tyr	Leu	Leu	Pro	Val	
W-->	332			615							620				625			
	334	GCT	GTG	GTG	AGC	CTG	GCC	TAC	GGG	CGC	ACG	CTG	CGC	TTC	CTG	TGG	GCC	816
	335	Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	Leu	Arg	Phe	Leu	Trp	Ala	
W-->	336			630					635					640				
	338	GCC	GTG	GGT	CCC	GCG	GGC	GCG	GCG	GCG	GCC	GAG	GCG	CGG	CGG	AGG	GCG	864
	339	Ala	Val	Gly	Pro	Ala	Gly	Ala	Ala	Ala	Ala	Glu	Ala	Arg	Arg	Arg	Ala	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,343

DATE: 02/01/2002

TIME: 11:47:31

Input Set : N:\Crf3\RULE60\10006343.raw

Output Set: N:\CRF3\02012002\J006343.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:58 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:261 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:296 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:578 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:593 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:610 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
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L:761 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:776 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,343

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TIME: 11:47:31

Input Set : N:\Crif3\RULE60\10006343.raw

Output Set: N:\CRF3\02012002\J006343.raw

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L:854 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:869 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:884 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:899 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:914 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:929 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
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L:1063 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39
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L:1093 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41
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L:1123 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43
L:1138 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44
L:1153 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45
L:1168 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46
L:1183 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47
L:1201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48
L:1216 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49
L:1231 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50
L:1246 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51
L:1260 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52